CLAIMS

1. A method for detecting a neoplasia in a biologic sample, the method comprising quantifying the promoter methylation of at least two promoters in the sample, wherein one of the promoters is *pi-class glutathione S-transferase* (*GSTP1*) and the second promoter is selected from the group consisting of O^6-*methylguanine DNA methyltransferase* (*MGMT*), *p14/ARF*, *p16/INK4a*, *RAS-associated domain family 1A* (*RASSF1A*), *adenomatous polyposis coli* (*APC*), *tissue inhibitor of metalloproteinase-3* (*TIMP3*), *S100A2*, *cellular retinoid binding protein 1* (*CRBP1*), and *retinoic acid receptor β2* (*RARβ2*), wherein an increased quantity of promoter methylation relative to a reference indicates the presence of a neoplasia in the sample.

2. The method of claim 1, wherein the second promoter is selected from the group consisting of *APC*, *RASSF1A*, *CRBP1*, and *RARβ2*.

3. A method for detecting a neoplasia in a biologic sample, the method comprising quantifying the promoter methylation of a promoter selected from the group consisting of *MGMT*, *p14/ARF*, *p16/INK4a*, *APC*, *RASSF1A*, *TIMP3*, *S100A*, *CRBP1*, and *RARβ2* in the sample, wherein an increased quantity of promoter methylation relative to a reference indicates the presence of a neoplasia in the sample.

4. The method of claim 3, wherein the promoter is selected from the group consisting of *APC*, *RASSF1A*, *CRBP1*, and *RARβ2*.

5. A method of determining the clinical aggressiveness of a neoplasia in a biologic sample, the method comprising quantifying the level of *GSTP1* or *APC* promoter methylation in the sample, wherein an increased level of promoter methylation relative to a reference indicates an increased clinical aggressiveness of the neoplasia.

6. A method of determining the stage of a neoplasia in a biologic sample, the method comprising quantifying the level of promoter methylation in the sample of at least one promoter selected from the group consisting of *GSTP1*, *APC*, *RASSF1A*,

and *RARβ2*, wherein an increased level of promoter methylation in the sample relative to a reference indicates an increased stage of neoplasia.

7. The method of any one of claim 1-6, wherein the neoplasia is prostate cancer.

8. The method of any one of claims 1-6, wherein the biologic sample is a patient sample.

9. The method of claim 8, wherein the patient sample is a tissue sample.

10. The method of claim 9, wherein the tissue sample is a prostate tissue sample.

11. The method of claim 8, wherein the patient sample is a biologic fluid.

12. The method of claim 11, wherein the biologic fluid is selected from the group consisting of serum, plasma, ejaculate, or urine.

13. The method of any one of claims 1-6, wherein the reference is the level of methylation present at the promoter in a control sample.

14. The method of claim 13, wherein the control sample is derived from a healthy subject.

15. The method of any one of claims 1-6, wherein the promoter methylation is quantified by quantitative methylation-specific PCR (QMSP).

16. The method of claim 15, wherein the level of promoter methylation is quantified.

17. The method of claim 15, wherein the frequency of promoter methylation is quantified.

18. The method of any one of claims 1-6, wherein the methylation levels of the *GSTP1* and *APC* promoters are quantified.

19. The method of claim 18, wherein the combined use of the *GSTP1* and *APC* promoters results in at least 90% specificity.

20. The method of claim 18, wherein the combined use of the *GSTP1* and *APC* promoters results in at least 90% sensitivity.

21. The method of any one of claims 1-6, wherein the methylation levels of at least three promoters are quantified.

22. A method for detecting prostate cancer in a prostate tissue sample, the method comprising quantifying the promoter methylation of at least two promoters by QMSP in the sample, wherein one of the promoters is *GSTP1* and the second promoter is selected from the group consisting of *APC*, *RASSF1A*, *CRBP1*, and *RARβ2*, and wherein a significantly increased quantity of promoter methylation relative to a reference indicates the presence of prostate cancer in the tissue sample.

23. A method for detecting a prostate cancer in a prostate tissue sample, the method comprising quantifying the promoter methylation of at least two promoters by QMSP in the sample, wherein the promoters are selected from the group consisting of *APC*, *RASSF1A*, *CRBP1*, and *RARβ2*, and wherein an increased quantity of promoter methylation relative to a reference indicates the presence of prostate cancer in the sample.

24. A method of determining the clinical aggressiveness of a prostate cancer in a prostate tissue sample, the method comprising quantifying the level of *GSTP1* or *APC* promoter methylation in the sample using QMSP, wherein an increased level of promoter methylation relative to a reference indicates an increased clinical aggressiveness of neoplasia.

25. A method of determining the stage of a prostate cancer in a prostate tissue sample, the method comprising quantifying the level of promoter methylation

in the sample of at least one promoter selected from the group consisting of *GSTP1*, *APC*, *RASSF1A*, and *RARβ2*, wherein an increased level of promoter methylation in the sample relative to a reference indicates an increased stage of prostate cancer.

26. The method of any one of claims 1-25, wherein the level of promoter methylation has a cutoff value of 1.

27. The method of any one of claims 1-25, wherein the level of promoter methylation has a cutoff value of 2.

28. The method of any one of claims 1-25, wherein the level of promoter methylation has a cutoff value of 3.

29. The method of any one of claims 1-25, wherein the level of promoter methylation has a cutoff value of 4.

30. The method of any one of claims 1-25, wherein the level of promoter methylation has a cutoff value of 5.

31. A method of diagnosing a subject as having a neoplasia, the method comprising quantifying the level of promoter methylation in a sample derived from the subject, wherein at least one promoter is selected from the group consisting of *GSTP1*, *APC*, *RASSF1A*, *CRBP1*, and *RARβ2*, and wherein an increased level of methylation relative to a reference indicates that the subject has a neoplasia.

32. The method of claim 31, wherein the level of promoter methylation has a cutoff value of 1.

33. The method of claim 31, wherein the level of promoter methylation has a cutoff value of 2.

34. The method of claim 31, wherein the level of promoter methylation has a cutoff value of 3.

35. The method of claim 31, wherein the level of promoter methylation has a cutoff value of 4.

36. The method of claim 31, wherein the level of promoter methylation has a cutoff value of 5.

37. A method of determining the prognosis of a subject diagnosed as having a neoplasia, the method comprising quantifying the level of promoter methylation in a sample derived from the subject, wherein at least one promoter is selected from the group consisting of *GSTP1*, *APC*, *RASSF1A*, *CRBP1*, and *RARβ2*, and wherein an altered level of promoter methylation relative to a reference indicates the prognosis of the subject.

38. The method of claim 37, wherein the alteration is a decrease in the level of promoter methylation relative to a reference.

39. The method of claim 38, wherein the decreased level of promoter methylation indicates a poor prognosis.

40. The method of claim 38, wherein the decreased level of promoter methylation indicates a good prognosis.

41. The method of claim 37, wherein the alteration is an increase in the level of promoter methylation relative to a reference.

42. The method of claim 41, wherein the increased level of promoter methylation indicates a poor prognosis for the subject.

43. The method of claim 41, wherein the increased level of promoter methylation indicates a good prognosis for the subject.

44. A method of monitoring a subject diagnosed as having a neoplasia, the method comprising quantifying the level of promoter methylation in a sample derived from the subject, wherein at least one promoter is selected from the group consisting

of *GSTP1*, *APC*, *RASSF1A*, *CRBP1*, and *RARβ2*, and wherein an altered level of promoter methylation relative to the level of methylation in a reference indicates an altered severity of neoplasia in the subject.

45. The method of any one of claims 22-44, wherein the reference is the level of methylation present in a sample previously obtained from the subject.

46. The method of any one of claims 22-44, wherein the reference is a baseline level of methylation present in a sample from the subject obtained prior to therapy.

47. The method of any one of claims 37-44, wherein the reference is the level of methylation present in a normal patient sample.

48. The method of any one of claims 22-44, wherein the subject is a human patient.

49. The method of claim 49, wherein the patient sample is a tissue sample.

50. The method of claim 50, wherein the tissue sample is a prostate tissue sample.

51. The method of claim 49, wherein the patient sample is a biologic fluid.

52. The method of claim 51, wherein the biologic fluid is selected from the group consisting of serum, plasma, ejaculate, or urine.

53. The method of any one of claims 22-52, wherein the promoter methylation is quantified by quantitative methylation-specific PCR.

54. The method of claim 53, wherein the level of promoter methylation is quantified.

55. The method of claim 53, wherein the frequency of promoter methylation is quantified.

56. The method of any one of claims 20-43, wherein the methylation levels of the *GSTP1* and *APC* promoters are quantified.

57. The method of any one of claims 20-56, wherein the methylation levels of at least three promoters are quantified.

58. A method of selecting a treatment for a subject diagnosed as having a neoplasia, the method comprising:

(a) quantifying the level of promoter methylation in a biologic sample from the subject relative to a reference, wherein the level of promoter methylation is indicative of a treatment; and

(b) selecting a treatment.

59. The method of any one of claims 22-58, wherein the neoplasia is prostate cancer.

60. A method of selecting a treatment for a subject diagnosed as having prostate cancer, the method comprising:

(a) quantifying the level of promoter methylation of a promoter selected from the group consisting of *GSTP1*, *APC*, *RASSF1A*, *CRBP1*, and *RARβ2* in a subject sample; and

(b) selecting a treatment for the subject, wherein the treatment is selected from the group consisting of surveillance, surgery, hormone therapy, chemotherapy, and radiotherapy.

61. A method for determining the methylation profile of a prostate cancer, the method comprising quantifying the level of promoter methylation at two or more promoters selected from the group consisting of *GSTP1*, *APC*, *RASSF1A*, *CRBP1*, and *RARβ2* in a biologic sample, wherein the level of promoter methylation relative to a reference determines the methylation profile of the prostatic neoplasia.

62. A kit for the analysis of promoter methylation, the kit comprising at least one primer capable of distinguishing between methylated and unmethylated promoter sequences, wherein the promoter sequences are selected from the group consisting of *GSTP1*, *APC*, *RASSF1A*, *CRBP1*, and *RARβ2*, and directions for using the primer for the analysis of promoter methylation.

63. A kit for the analysis of promoter methylation, the kit comprising at least one pair of primers capable of amplifying a promoter sequence selected from the group consisting of *GSTP1*, *APC*, *RASSF1A*, *CRBP1*, and *RARβ2*, wherein at least one of the primers binds selectively to a methylated or unmethylated sequence.

64. The kit of claim 62 or 63, further comprising a pair of primers for amplifying the promoter sequence of a reference gene.

65. The kit of claim 62 or 63, wherein the reference gene is ACTB.

66. The kit of claim 62 or 63, further comprising a detectable probe, wherein the probe is capable of binding to the promoter sequence.

67. The kit of claim 66, wherein the probe is detected by fluorescence, by autoradiography, by an immunoassay, by an enzymatic assay, or by a colorimetric assay.

68. The kit of claim 62 or 63, further comprising a reagent that converts methylated cytosine to uracil.

69. A microarray comprising at least two nucleic acid molecules, or fragments thereof, bound to a solid support, wherein the two nucleic acid molecules are selected from the group consisting of *GSTP1*, *MGMT*, *p14/ARF*, *p16/INK4a*, *APC*, *RASSF1A*, *TIMP3*, *S100A*, *CRBP1*, and *RARβ2*.

70. A method for detecting a neoplasia in a biologic sample, the method comprising quantifying the promoter methylation of at least two promoters in the sample by contacting the sample with a microarray of claim 59, wherein one of the

promoters is selected from the group consisting of *GSTP1*, *MGMT*, *p14/ARF*, *p16/INK4a*, *APC*, *RASSF1A*, *TIMP3*, *S100A*, *CRBP1*, and *RARβ2*, and wherein an increased quantity of promoter methylation relative to a reference indicates the presence of a neoplasia in the sample.

71. A primer having a nucleic acid sequence selected from the group consisting of:

5'- TGG TTT CGA TTT TTT GAT TTC G -3' (SEQ ID NO:1).

5'- TCA AAA TTC TTT TTA CAA CAA CGC C -3' (SEQ ID NO:2),

5'- CTG GGA ATC CAG CTG TCG CCG CCC CGC A -3' (SEQ ID NO:4),

5'- GCG CAT CAT AGC CAT CAG CAA CAA A -3' (SEQ ID NO:5),

5'-CGA GAA CGC GAG CGA TTC-3' (SEQ ID NO:7),

5'-CAA ACT TAC TCG ACC AAT CCA ACC-3' (SEQ ID NO:8),

5'-TGG TGA TGG AGG AGG TTT AGT AAG T-3' (SEQ ID NO:10)

5'- AAC CAA TAA AAC CTA CTC CTC CCT TAA-3'(SEQ ID NO:11).

72. A probe having a nucleic acid sequence selected from the group consisting of:

5'- CGA CCG AAC GCG ATA ACT TAC TCC -3'-TAMRA (SEQ ID NO:3),

5'- GAC CCG AAA ATA AAC GCC CTC CGA AAA CA -3' (SEQ ID NO:6),

5'-TCG GAA CGT ATT CGG AAG GTT TTT TGT AAG TAT TT-3' (SEQ ID NO:9),

5'-ACC ACC ACC CAA CAC ACA ATA ACA AAC ACA-3' (SEQ ID NO:12).

73. A collection of primer sets, each of the primer sets comprising at least two primers that bind to a promoter selected from the group consisting of *GSTP1*, *MGMT*, *p14/ARF*, *p16/INK4a*, *APC*, *RASSF1A*, *TIMP3*, *S100A*, *CRBP1*, and *RARβ2*, the collection comprising at least two primer sets.